Draft Assembly Improvement

- **Motivation and background**
- **Goals and objectives**
- **Methods**
- **Results and discussion**
- **Still to do**

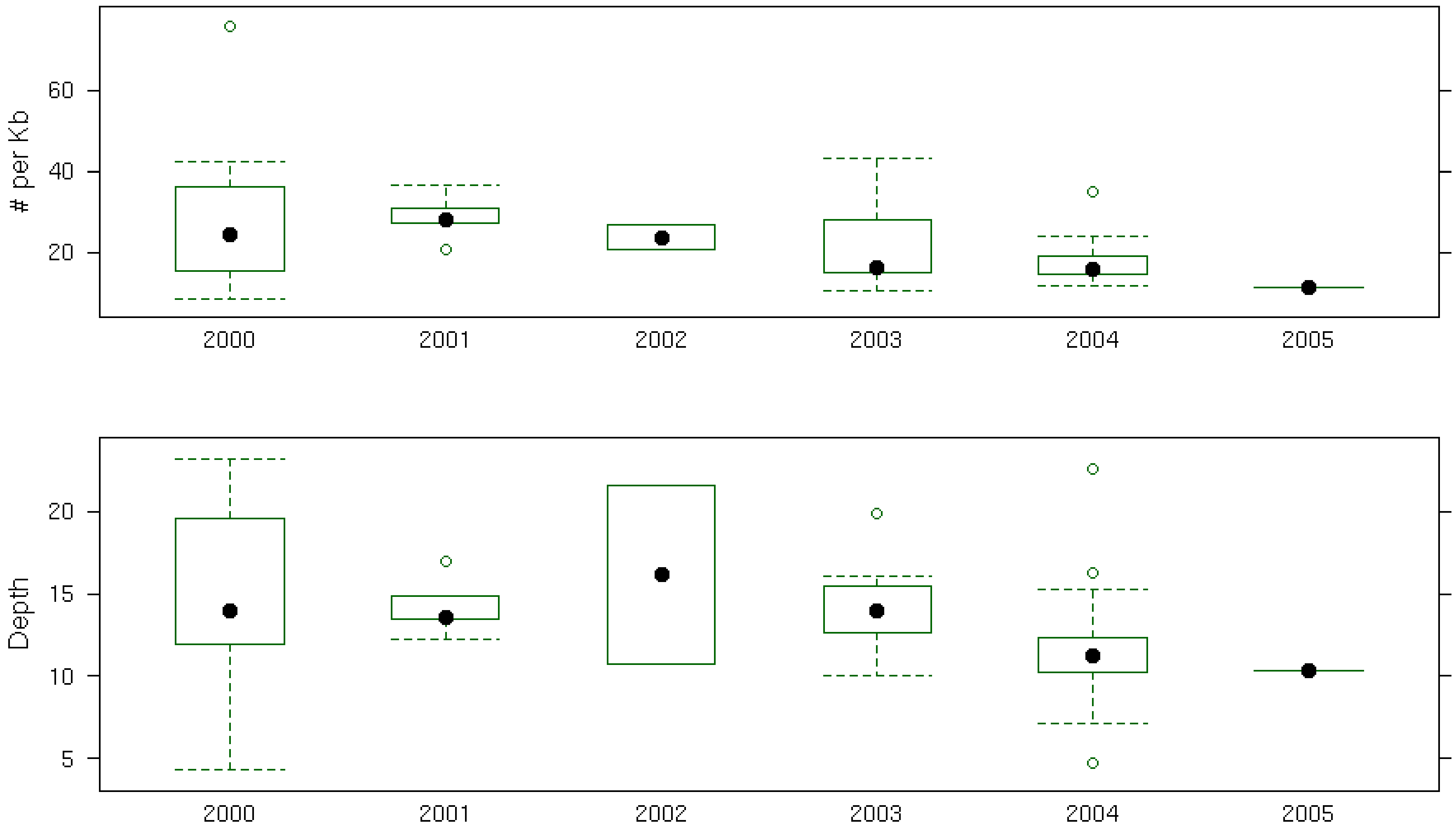
History

- **Early projects contaminated**
  - **Some assemblies failed to complete**
  - **Many long running assemblies**
  - **Lots of ad-hoc repairs and clean up**
- **Sequenced more reads than needed**

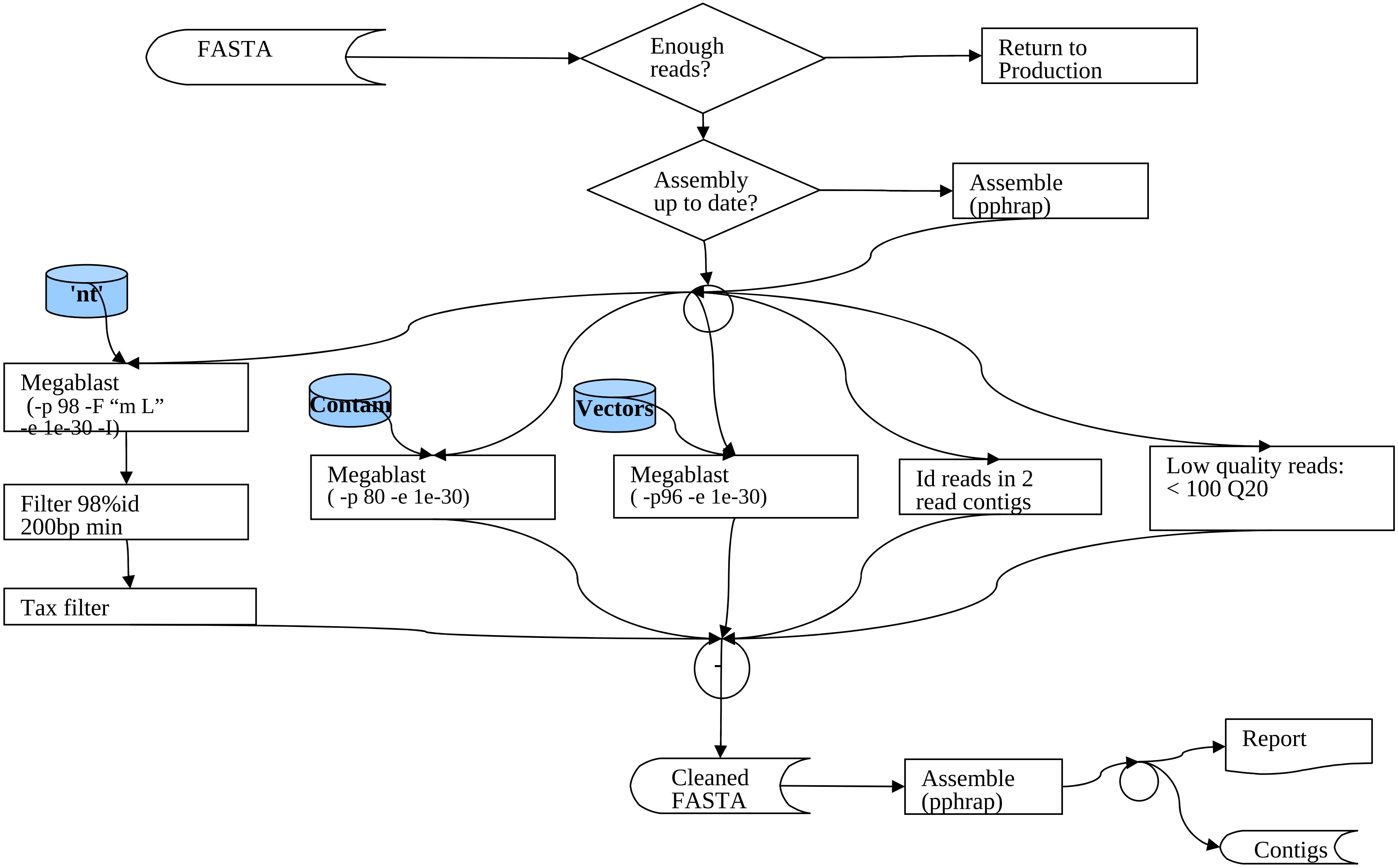
Goals

- **Do no harm**
- **Clean up obvious problems**
- **Make best use of existing data**
- **Create better assemblies for finishing**
- **Clean up public submissions**

Reads sequenced per 1000 bp of Genome



Flowchart



FASTA

Enough reads?

Return to Production

Assembly up to date?

Assemble (pphrap)

'nt'

Megablast (-p 98 -F “m L” -e 1e-30 -I)

Filter 98%id 200bp min

Tax filter

Contam

Megablast (-p 80 -e 1e-30)

Vectors

Megablast (-p96 -e 1e-30)

Id reads in 2 read contigs

Low quality reads: < 100 Q20

-

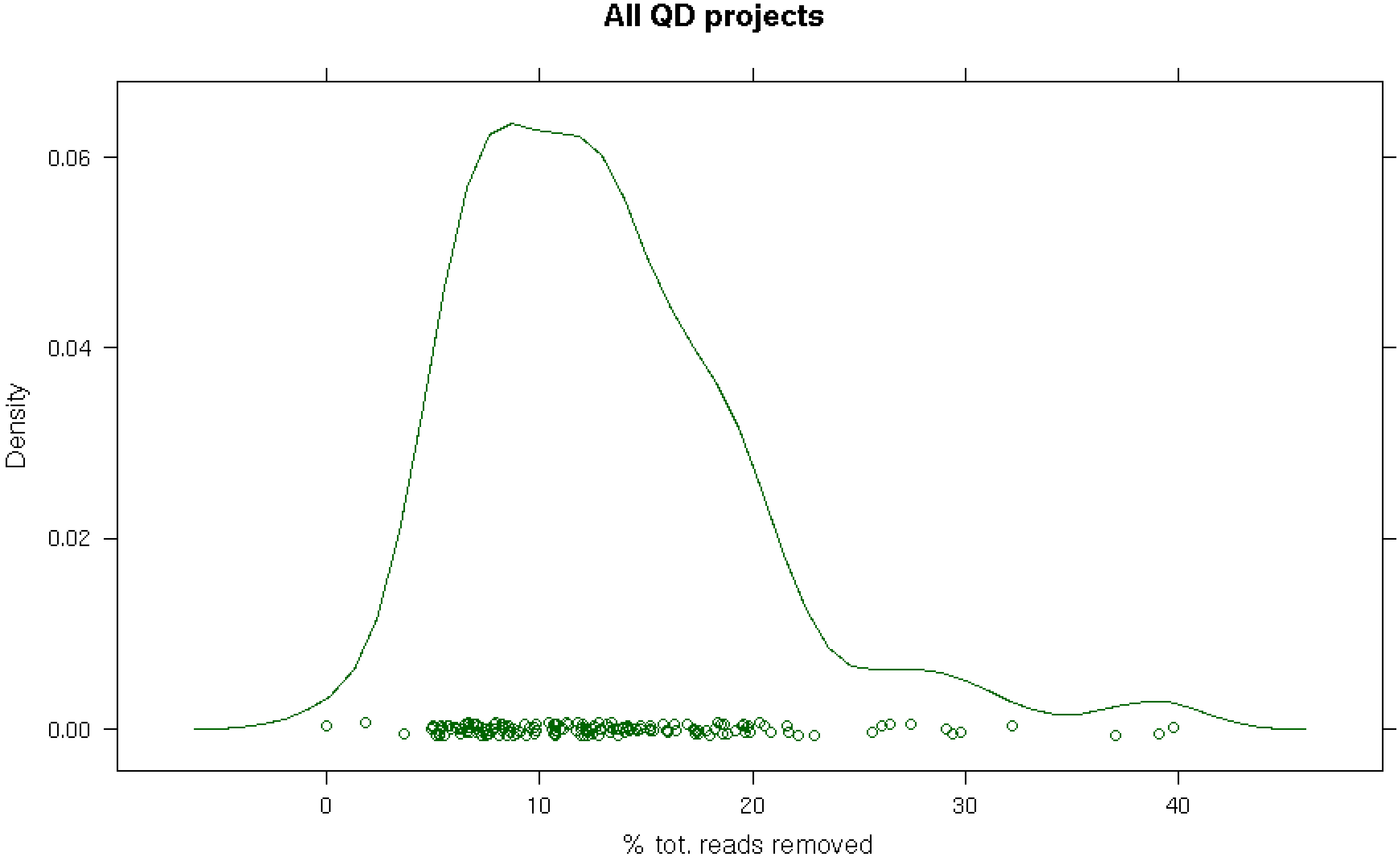
Cleaned FASTA

Assemble (pphrap)

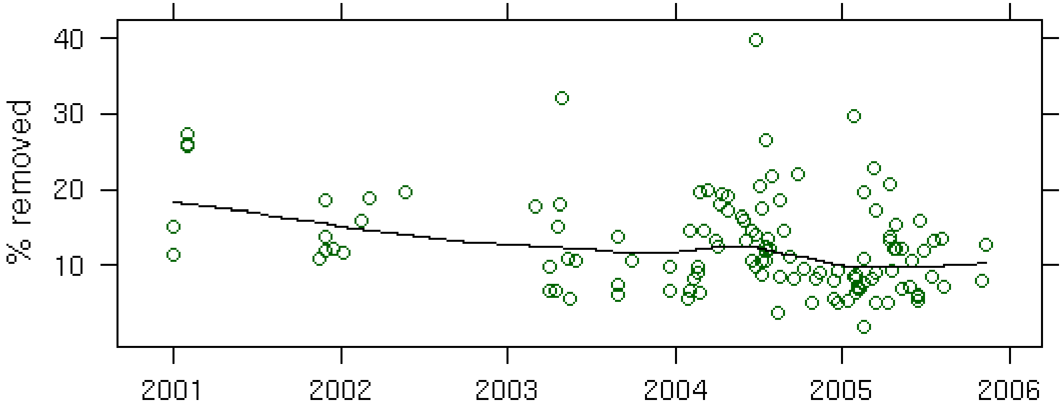
Report

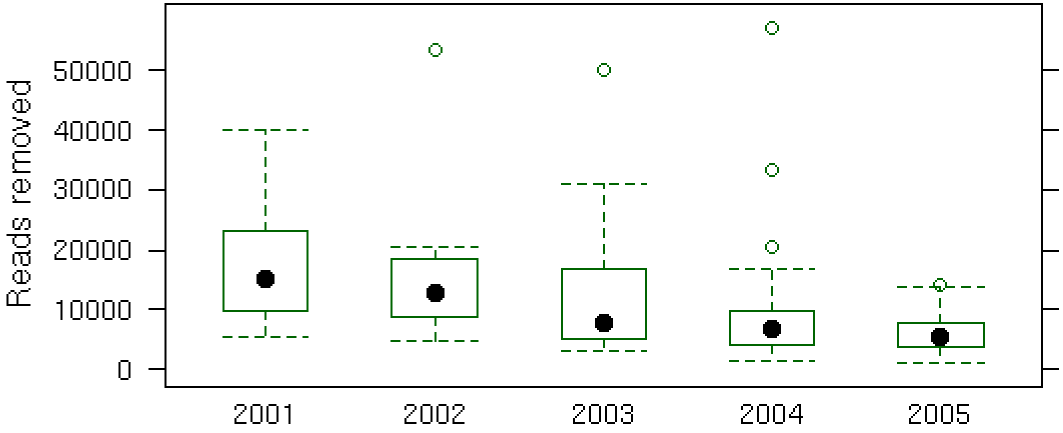
Contigs

What's not used



Process improvement ?





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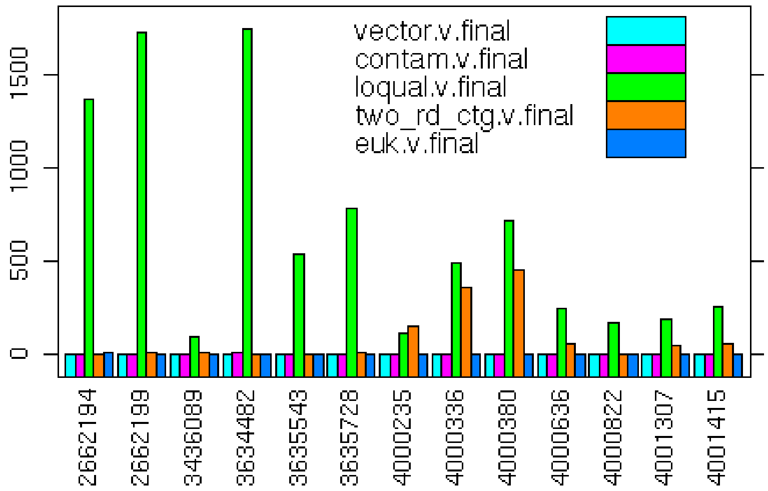
Breakdown of removed reads mapped to finished genomes

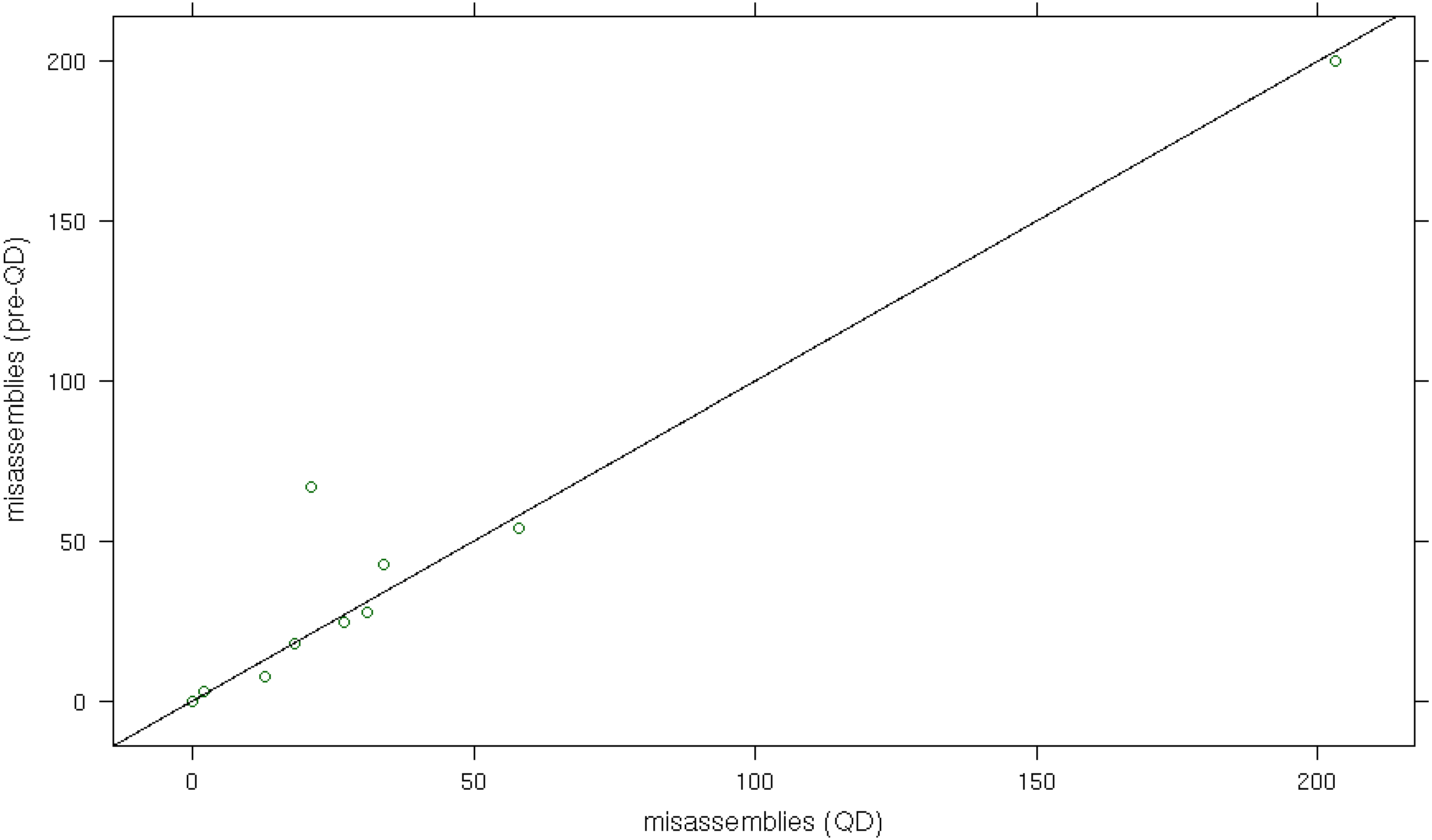
% removed with BLAST hits to finishe				Breakdown of removed reads				# removed reads hitting finished				
Low Quality	2 Rd Contig	Contam.	Euk.	Low Qual.	2 Rd Contig	Contam.	Euk.	loqual.v.final	2 Rd Ctg.v.final	contam.v.final	euk.v.final	vector.v.final
10.4	0.0	1.1	41.7	13146	5	280	12	1367	0	3	5	1
12.5	0.9	0.0	0.0	13832	436	324	98	1730	4	0	0	0
2.8	3.5	1/0	1/0	3353	144		0	94	5	0	0	0
14.8	1/0	1.7	0.7	11862	0	352	144	1750	0	6	1	0
16.4	13.6	1/0	1/0	3249	22	0	0	532	3	0	0	0
18.2	0.4	1/0	1/0	4274	1632	0	0	778	7	0	0	0
2.0	28.3	0.0	0.0	5349	519	2	3	107	147	0	0	0
6.8	62.4	0.0	1/0	7172	577	4	0	485	360	0	0	0
8.0	22.2	0.0	0.0	8955	2027	49	7	720	450	0	0	1
22.7	68.4	1/0	0.0	1071	76	0	20	243	52	0	0	0
25.8	1/0	1/0	0.0	647	0	0	1	167	0	0	0	0
19.4	91.1	0.0	1/0	943	45	2	0	183	41	0	0	0
27.5	73.0	0.0	1/0	936	74	2	0	257	54	0	0	0

Do removed reads belong?

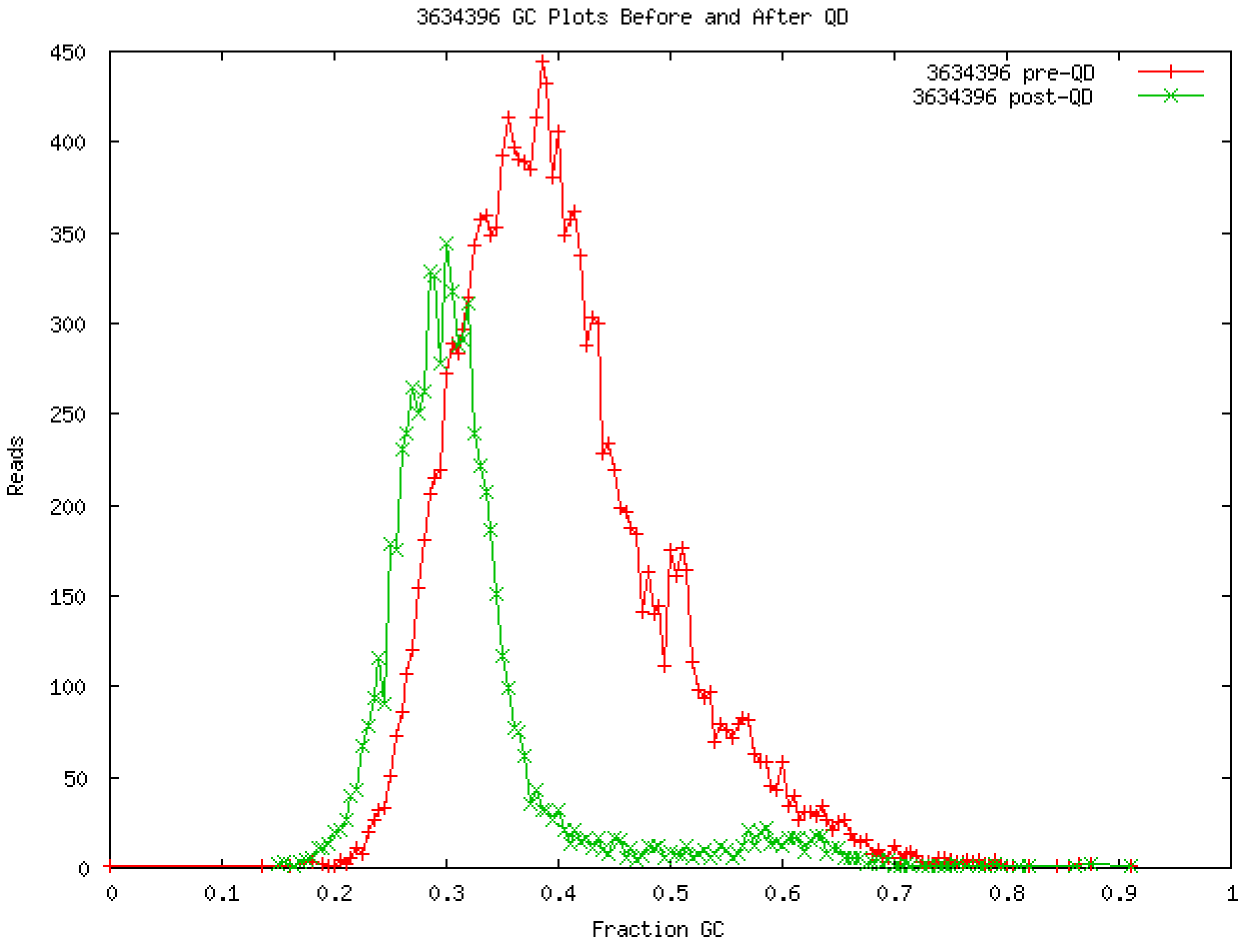


- Examined 14 finished projects
- BLAST removed reads against finished
- ~ 20% of low quality hit finished
- 2-read contigs are variable

Misassemblies



Benefits of QD



Summary

- **195 projects**
- **Projects appear to be improving**
- **Examined 14 finished projects – some number of removed reads belong in project**

Todo

- **Low quality filter could use tuning**
- **Better organism selectivity**

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